Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

NM 022162:Homo sapiens nucleotide-binding...SEQ ID NO: 1

Results for: ref|NM_022162.1 Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA(4485bp) Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|11545911|ref|NM_022162.1|

Description

Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA

Molecule type

rna

Query Length

4485

Subject ID

42571

Description

None

Molecule type

nucleic acid

Subject Length

20

Program

BLASTN 2.2.20+ Citation

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Other reports: Search Summary [Taxonomy reports]

Program	blastn
Word size	11
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
Н	0.912438	0.78

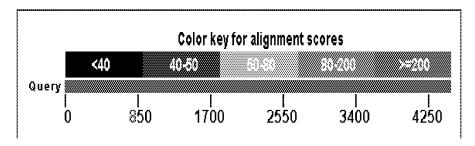
Results Statistics

Effective search space 44750

Graphic Summary

Distribution of 1 Blast Hits on the Query Sequence

[?]



Plot of gi|11545911|ref|NM_022162.1| vs 42571 [2]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

42571 37.4 37.4 0% 3e-07 100%

Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

NM 022162:Homo sapiens nucleotide-binding...SEQ ID NO: 2

Results for: ref|NM_022162.1 Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA(4485bp)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|11545911|ref|NM_022162.1|

Description

Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA

Molecule type

rna

Query Length

4485

Subject ID

1677

Description

None

Molecule type

nucleic acid

Subject Length

20

Program

BLASTN 2.2.20+ Citation

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Other reports: Search Summary [Taxonomy reports]

Program	blastn
Word size	11
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
Н	0.912438	0.78

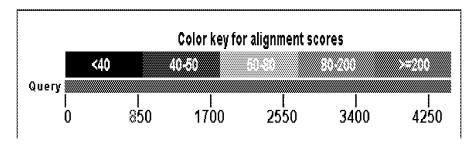
Results Statistics

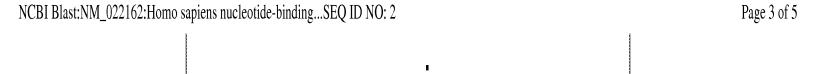
Effective search space 44750

Graphic Summary

Distribution of 1 Blast Hits on the Query Sequence

[?]





Plot of gi|11545911|ref|NM_022162.1| vs 1677 [2]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

1677 37.4 37.4 0% 3e-07 100%

•

Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

NM 022162:Homo sapiens nucleotide-binding...SEQ ID NO:5

Results for: *ref|NM_022162.1 Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA(4485bp) Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|11545911|ref|NM_022162.1|

Description

Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA

Molecule type

rna

Query Length

4485

Subject ID

26991

Description

None

Molecule type

nucleic acid

Subject Length

26

Program

BLASTN 2.2.20+ Citation

Reference

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

• No significant similarity found. For reasons why, click here

Other reports: Search Summary [Taxonomy reports]

Search Parameters

Program	blastr
Word size	11
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1
Template length	18
Window Size	40

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
Н	0.912438	0.78

Results Statistics

Effective search space 67110

Graphic Summary

Distribution of Blast Hits on the Query Sequence

[?]

Descriptions

Alignments

Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

NM 022162:Homo sapiens nucleotide-binding...SEQ ID NO:6

Results for: ref|NM_022162.1 Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA(4485bp)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|11545911|ref|NM_022162.1|

Description

Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA

Molecule type

rna

Query Length

4485

Subject ID

17521

Description

None

Molecule type

nucleic acid

Subject Length

20

Program

BLASTN 2.2.20+ Citation

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Other reports: Search Summary [Taxonomy reports]

Program	blastn
Word size	11
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
Н	0.912438	0.78

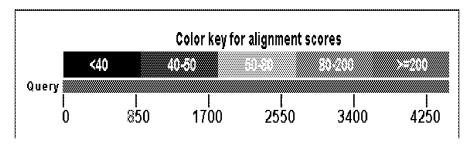
Results Statistics

Effective search space 44750

Graphic Summary

Distribution of 1 Blast Hits on the Query Sequence

[?]





Plot of gi|11545911|ref|NM_022162.1| vs 17521 [2]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

17521 37.4 37.4 0% 3e-07 100%

Blast 2 sequences

Edit and Resubmit Save Search Strategies Formatting options Download

NM 022162:Homo sapiens nucleotide-binding...SEQ ID NO:9

Results for: ref|NM_022162.1 Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA(4485bp) Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|11545911|ref|NM_022162.1|

Description

Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA

Molecule type

rna

Query Length

4485

Subject ID

53501

Description

None

Molecule type

nucleic acid

Subject Length

26

Program

BLASTN 2.2.20+ Citation

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Other reports: Search Summary [Taxonomy reports]

Program	blastn
Word size	11
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
Н	0.912438	0.78

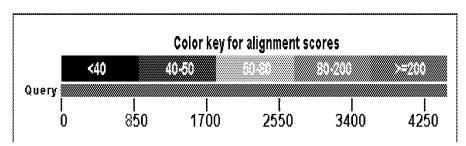
Results Statistics

Effective search space 67110

Graphic Summary

Distribution of 1 Blast Hits on the Query Sequence

[?]



Plot of gi|11545911|ref|NM_022162.1| vs 53501 (2)

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

53501 48.2 48.2 0% 2e-10 100%

Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

NM 022162:Homo sapiens nucleotide-binding...SEQ ID NO:10

Results for: ref|NM_022162.1 Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA(4485bp)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|11545911|ref|NM_022162.1|

Description

Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA

Molecule type

rna

Query Length

4485

Subject ID

691

Description

None

Molecule type

nucleic acid

Subject Length

24

Program

BLASTN 2.2.20+ Citation

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Other reports: Search Summary [Taxonomy reports]

Program	blastn
Word size	11
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
Н	0.912438	0.78

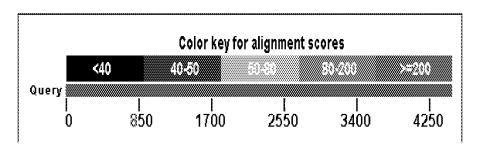
Results Statistics

Effective search space 62650

Graphic Summary

Distribution of 2 Blast Hits on the Query Sequence

[?]





Plot of gi|11545911|ref|NM_022162.1| vs 691 [2]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

691 37.4 60.3 0% 4e-07 100%

```
>lcl|691
Length=24
```

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position